

# HUMAN xiap

SEQ ID NO:3 1 gaaaagggtggacaaggtaattcaagaagatgactttaaacagtttgaaggatct  
SEQ ID NO:4 a . M T F N S F E G S - 60  
a  
61 aaaacttgtgtacacctgcagacatcaataaggaaagaatggtaagaaggataga  
a  
K T C V P A D I N K E E F V E E F N R - 120  
ttaaaaactttgctaatttcaagaatgtgttagtcctgttcagcatcaacactggcacga  
a  
L K T F A N F P S G S P V S A S T L A R - 180  
gcagggttttataactgggtgaaaggataccgtgcgggtcgatgtcatgcagt  
181  
a  
A G F L Y T G E G D T V R C F S C H A A - 240  
gtagatagatggcaatatggagactcagcagttgaaagacacagggaaagtatccaaat  
241  
a  
V D R W Q Y G D S A V G R H R K V S P N - 300  
tgcagatttatcaacgggtttatcttgcggaaatagtgccacggcagttacaattcttgt  
301  
a  
C R F I N G F Y L E N S A T Q S T N S G - 360

Fig. 1 (page 1 of 7)



## HUMAN xiap

361 atccagaatggcagtaaactatctggaaagcagagatcatttgactta  
a I Q N G Q Y K V E N Y L G S R D H F A L - 420  
gacaggccatctgagacacatgcagactatctttgagaactggcagggttagata  
421 a D R P S E T H A D Y L L R T G Q V V D I - 480  
tcagacaccatacccgaggaacctgtcatgtttagaaagactagatcaaagttcc  
481 a S D T I Y P R N P A M Y C E E A R L K S - 540  
tttcagaactggccagactatgctcacctaacccaaagagatgttagcaagtgtggactc  
541 a F Q N W P D Y A H L T P R E L A S A G L - 600  
tactacacaggtattggtagccaagtgcatgtgtttgtggaaaactgaaaaat  
601 a Y Y T G I G D Q V Q C F C C G G K L K N - 660  
tggaaaccttgtgatcgtgcctggcagaacacaggcgacactttcttaattgttttt  
661 a W E P C D R A W S E H R R H F P N C F F - 720

Fig. 1 (page 2 of 7)

## HUMAN xiap

721 gttttggccggaatcttaatattcgaagtgaatctgatgtgagttctgataggaat 780  
a v L G R N L N I R S E S D A V S S D R N -  
ttcccaaattcaacaatcttccaagaatccatccatggcagattatggacacggatc  
781 -+-----+-----+-----+-----+-----+-----+-----+-----+ 840  
a F P N S T N L P R N P S M A D Y E A R I -  
tttactttggacatggatatactcagttacaacaaggaggcagactggattt 900  
a F T F G T W I Y S V N K E Q L A R A G F -  
tagcttttaggtgataaagtaagtgctttactgtggaggaggctaaactgtat 960  
901 -+-----+-----+-----+-----+-----+-----+-----+-----+ 960  
a Y A I G E D K V K C F H C G G G L T D -  
tggaaaggccagtgaagacccttggaaacaacatgcttaatggatccagggtgcaaatat  
961 -+-----+-----+-----+-----+-----+-----+-----+-----+ 1020  
a W K P S E D P W E Q H A K W Y P G C K Y -  
ctgttagaacaaggacaagaataataacaatattcatttaactcattcaacttgag  
1021 -+-----+-----+-----+-----+-----+-----+-----+-----+ 1080  
a I L E Q K G Q E Y I N N I H L T H S L E -

Fig. 1 (page 3 of 7)

## HUMAN xiap

1081 gagtgtctggttaagaactactgagaaaaacaccatcaactagaagaattgatgatacc  
-+-----+-----+-----+-----+-----+-----+-----+-----+ 1140  
a E C I V R T T E K T P S L T R R I D D T -  
atcttccaaaatcctatggtaacaagaagctatacgaatgggttcagttcaaggacatt  
-+-----+-----+-----+-----+-----+-----+-----+-----+ 1200  
a I F Q N P M V Q E A I R M G F S F K D I -  
aagaaaaataatggagaaaaattcagatatctggagcaactataatcacttgagtt  
-+-----+-----+-----+-----+-----+-----+-----+-----+ 1260  
1261 K K I M E E K I Q I S G S N Y K S L E V -  
ctgggtgcagatctatgtgaatgctcagaagacagatgtcaagatgagtcagact  
-+-----+-----+-----+-----+-----+-----+-----+-----+ 1320  
a L V A D L V N A Q K D S M Q D E S S Q T -  
tcattacagaagagattactgaagagcagctaaggccgtgcaagaggagaagtt  
-+-----+-----+-----+-----+-----+-----+-----+-----+ 1380  
1321 a S I Q K E I S T E E Q L R R L Q E E K L -  
tgcaaaatctgtatggatagaatattgctatcggtttgtcttgacatctagtc  
-+-----+-----+-----+-----+-----+-----+-----+-----+ 1440  
1381

Fig. 1 (page 4 of 7)

# HUMAN xiap

a C K I C M D R N I A I V F V P C G H L V -  
1441 acttgtaaaatgtgtctgaaagcagttacaagtgccatgtgttacact 1500  
a T C K Q C A E A V D K C P M C Y T V I T -  
1501 ttcagaacaaattttatgtcttaatctaactctatagtaggcattatgtgttct 1560  
a F K Q K I F M S \* -  
1561 tattaccctgattgaatgtgtgtactttaagtaatcaggattgaattccat 1620  
a -  
1621 tagcatttgctaccaggaaaaatgtacatggcagtggttttagtggcaatata 1680  
a -  
1681 atctttgaaattttgtttttcagggtatttagtattatccatttttactgtta 1740  
a -  
1741 tttaattgaaaccatagaactaagaataagaagcatactataactgaacacaatgtgt 1800  
a -

Fig. 1 (page 5 of 7)

## HUMAN xiap

1801 attccatagataactgatttaaattctaagtgtaaatcatctggattttat 1860  
a -  
1861 tctttcagataggcttaacaatggagcttctgtatataatgtggagattagat 1920  
a -  
1921 atctccccaaatcacataatttgtttgtgtgaaaaggaataaattgttccatgctgg 1980  
a -  
1981 gaaagatagatgttttagaggtgggtgtgttttaggattctgtccatttat 2040  
a -  
2041 tgtaaaagnataaacacgnacntgtgcgaatataatnttgcgtaaatggat 2100  
a -  
2101 aaagcgtattaatgatagaatactatcgaggccaacatgtactgacatggaaagatgtca 2160  
a -

Fig. 1 (page 6 of 7)

## HUMAN xiap

2161 nagatatgttaagtgtaaaatgc  
a aactgaggcnnacactatgtgatgtc  
2221 aagtatgtatgtnttaatgc  
a aatacagaacnana  
2281 ttaaatgtgtttcttcggggggggat  
a tgggggggggggggggggggggggg  
2341 naggcatttcactttcnacttttcatttt  
a cattttgttcgttctgttgc  
2401 nattttataagt  
a  
2461 gtanacccnaagggtttatgna  
a acatcagtaacctaacc  
2521 gtnctttcttagggagctgtnttgc  
a  
2540 ctgagtgtggggacttn

Fig. 1 (page 7 of 7)

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Fig. 2 (page 2 of 8)

## HUMAN hiap-1

CATGCCATTGACTTCTGTCGCCACAGATCTGGCACGGCAGGCTTACTACAG  
721 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 780  
C W P L T F L S P T D L A R A G F Y Y I G -  
GACCTGGAGACAGAGTGCTTGCTTGCCCTGTGGAAATTGAGCAATTGGAACCGA  
781 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 840  
C P G D R V A C F A C G G K L S N W E P K -  
AGGATAATGCTATGTCAGAACACCTGAGACATTTCCCAAATGCCATTATAGAAATC  
841 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 900  
C D N A M S E H L R H F P K C P F I E N Q -  
AGCTTCAAGACACTCAAGATAACAGAGTTCTAATCTGAGCATGCCAGACACATGCC  
901 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 960  
C L Q D T S R Y T V S N L S M Q T H A A R -  
GCTTTAACATTCTTAACGGCCCTCTAGTGTCTAGTTAACCTGAGCAGCTTGCAA  
961 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020  
C F K T F F N W P S S V L V N P E Q L A S -  
GTGCGGGTTTTATTATGCGGTAACAGTGATGTCATGCTTTGCTGTGATGGTG  
1021 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080  
C A G F Y V G N S D D V K C F C C D G G -

Fig. 2 (page 3 of 8)

## HUMAN hiap-1

1081 GACTCAGGTGTTGGAATCTGGAGATCCATGGGTCAACATGCCAAGTGGTTCCAA 1140  
c L R C W E S G D D P W V Q H A K W F P R -  
1141 GGTGTGAGTACTTGATAAGAATTAAAGGACAGGAGTTCATCCGTCAAGTTCAGGAGTT 1200  
c C E Y L I R I K G Q E F I R Q V Q A S Y -  
1201 ACCCTCATCTACTTGAAACAGCTGCTATCCACATCAGACAGCCCAGGAGATGAAATGCAG 1260  
c P H L L E Q L L S T S D S P G D E N A E -  
1261 AGTCATCAATTATCCATTGGAACCTGGAGAACGACATTAGAAGAGATGCAATCATGATGA 1320  
c S S I I H L E P G E D H S E D A I M M N -  
1321 ATACTCCTGTGATTAATGCTGCCGGAAATGGCCTTAGTAGAAGGCCTGGTAAACAGA 1380  
c T P V I N A A V E M G F S R S L V K Q T -  
1381 CAGTTCAAGAGAAAATCCTAGCAACTGGGAGAACATAAGACTAGTCATGATCTGTGT 1440  
c V Q R K I L A T G E N V R L V N D L V L -

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## HUMAN hiap-1

1441 TAGACTTACTCAATGCCAGAACGATGAAATAAGGGAAGAGGAAAGAGCAACTGAGG 1500  
c D L L N A E D E I R E E E R E R A T E E -  
1501 AAAAGAACATCAAATGATTATTAAATCCGGAAGAACATGGCACTTTCAACATT 1560  
c K E S N D L L I R K N R M A L F Q H L -  
1561 T G A C T T G T G T G A A T T C C A A T C C T G G A T A G T C T A C T A A C T G C C G G A T T A A T G A A C A C A G 1620  
c T C V I P I L D S L L T A G I I N E Q E -  
1621 A A C A T G A T G T T A T T A A C A C A G A G A C A C A G A C A G C T T A C A A G G A A G A A C T G A T T G A T A 1680  
c H D V I K Q K T Q T S L Q A R E L I D T -  
1681 C G A T T T A G T A A A G G A A T A T G C A G C C A C T G T A T T C A G A A A C T C T C T G C A A G A A G C T G 1740  
c I L V K G N I A A A T V F R N S L Q E A E -  
1741 A A G C T G T G T T A T A T G A G C A T T A T G C A C A G C A C A T A A A T A T A T C C C A C A G A A G 1800  
c A V L Y E H L F V Q Q D I K Y I P T E D -

Fig. 2 (page 5 of 8)

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Fig. 2 (page 6 of 8)

# HUMAN hiap-1

2161 TGAACATATTTAGAACTAAGAGAATGATAGGCTTGTCTATGAA~~CGAAA~~ 2220  
C -  
2221 GAGGTAGCACTACAAACACAATTC~~CAA~~ATT~~C~~AGCATTGAAATGTAAGTG 2280  
C -  
2281 AAGTAAACTAAGATATTGAGTTAACCTTAAGAATTAAATATTGGCATGAC 2340  
C -  
2341 TAATACGGAACATGAAGCCAGGTGTGGTATGTACCTGTAGTCCCAGGGCTGAGGCA 2400  
C -  
2401 AGAGAAATTACTTGAGCCCAGGAGTTGAATCCATCCTGGGCAGCATACTGAGACCC~~T~~GCC 2460  
C -  
2461 TTTAAACGXACAGXACCAAA~~CC~~ACAC~~CC~~AGGGACACATTCTGTCT~~TT~~TGAT 2520  
C -

Fig. 2 (page 7 of 8)

## HUMAN hiap-1

2521 CAGTGTCTATACTCGAAGGGTGCATATGTTGAATCACATTAGGGACATGGTGT 2580

C

2581 TTTTATAAGAATTCTGTGAGXAAAATTAAAGCAACCAATTACTCTTAA 2640

C

2641 AAAAAAAACTCGAGGGCCCGTACCAAT 2676

C

Fig. 2 (page 8 of 8)

## HUMAN hiap-2

SEQ ID NO:7

1	TAGGTTACCTGAAAGAGTTACTACAACCCAAAGAGTTGTTCTAAGTAGTATCTTG	60
a	TAATTCAAGAGATACTCATCCTACCTGAATATAAACTGAGATAATCCAGTAAAGAAG	120
61	-	-
a	TGTAGTAATTCTACATAAGAGTCTATCATGATTCTTTGTGGTGAATCTTAGT	180
121	-	-
a	CATGTGAAGAAATTTCATGTGAATGTTTAGCTATCAAACAGTACTGTCACCTACTCATG	240
181	-	-
a	CACAAACTGCCTCCCAAAGACTTTCCCAAGGTCCCTCGTATCAAACATTAAGAGTATA	300
241	-	-
SEQ ID NO:8	H K T A S Q R L F P G P S Y Q N I K S I -	
a	ATGGAAGATAGCAGGATCTGTCAGATTGGACAAACAGCAACAAACAAAAATGAAGTAT	360
301	-	-
a	M E D S T I L S D W T N S N K Q K M K Y -	

Fig. 3 (page 1 of 7)

## HUMAN hiap-2

361 GACTTTCTGTAACCTACAGAATGTCTACATATTCAACTTCCCCGGGGTGCCT  
a D F S C E L Y R M S T Y S T F P A G V P - 420  
421 GTCTCAGAAAGGAGTCTGCTCGTGCCTGGTTTATTACTGGGTGAATGACAAGGTC  
a V S E R S L A R A G F Y Y T G V N D K V -  
481 AAATGCTTCTGTTGTGCCCTGATGCTGGATAACTGGAAACTAGGAGACAGTCCTATTCAA  
a K C F C C G L M L D N W K L G D S P I Q - 540  
541 AAGCATAAACAGCTATATCCTAGCTGTAGCTTATTCAGAATCTGGTTCAAGCTAGTCTG  
a K H K Q L Y P S C S F I Q N L V S A S L -  
601 GGATCCACCTCTAAGAATAACGTCTCCAATGAGAACAGTTGCACATCATTATCTCCC  
a G S T S K N T S P M R N S F A H S L S P - 660  
661 ACCTTGGAACATAGTAGCTGTCTAGTGGTCTACTCCAGCCTTCCAAACCTCTT  
a T L E H S S L F S G S Y S S L P P N P L - 720

Fig. 3 (page 2 of 7)

## HUMAN hiap-2

721 AATTCTAGAGCAGTTGAAGACCATCTCTCATCGAGGACTAACCCCTACAGTTATGCAATG 780  
a N S R A V E D I S S S R T N P V S Y A M -  
AGTACTGAAGGCCAGATTCTACCTACCATATGTGGCCATTAACTTTGTACCA 781 840  
a S T E E A R F L T Y H M W P L T F L S P -  
TCAGAATTGGCAAGAGCTGGTTTATTATAGGACCTGGAGATAGGGTAGGCCCTGCTT 841 900  
a S E L A R A G F Y Y I G P G D R V A C F -  
GCCTCTGGTGGGAAGCTCAGTAACCTGGAACCAAAGGATGCTATGTCAAGAACCGG 901 960  
a A C G G K L S N W E P K D D A M S E H R -  
AGGCATTTCCCAACTGTCATTTGGAAATTCTCTAGAAACTCTGAGGTTAGCATT 961 1020 1080  
a R H F P N C P F L E N S L E T L R F S I -  
TCAAATCTGAGGCATGCAGACACATGCAGCTCGAATGAGAACATTTATGTACTGGCCATCT 1021 1080  
a S N L S M Q T H A A R M R T F M Y W P S -

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## HUMAN hiap-2

1081 AGTGTCCAGTCAGCCTGAGCAGCTGCAAGTGCTGGTTTATTATGTTGGGTGGCAAT 1140  
a S V P V Q P E Q L A S A G F Y Y V V G R N -  
1141 GATGATGTCAAATGCTTGGTTGTGATGGTGCTTGAGGTGTTGGAATCTGGAGATGAT 1200  
a D D V K C F G C D G G L R C W E S G D D -  
1201 CCATGGGTAGAACATGCCAAGTGGTTCCAAGGTTGTGAGTTCTTGATACGAATGAAAGGC 1260  
a P W V E H A K W F P R C E F L I R M K G -  
1261 CAAGAGTTGTTGATGAGATTCAAGGTAGATATCCTCATCTTCTTGAAACAGCTGTTGCA 1320  
a Q E F V D E I Q G R Y P H L L E Q L L S -  
1321 ACTTCAGATACCACTGGAGAAGAAATGCTGACCCACCAATTTCATTGACCTGGA 1380  
a T S D T T G E E N A D P P I I H F G P G -  
1381 GAAAGTTCTCAGAAGATGCTGTCATGATAACACCTGTGGTTAACATGCTTGAA 1440  
a E S S S E D A V M M N T P V V K S A L E -

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Fig. 3 (page 5 of 7)

## HUMAN hiap-2

1801 AACATCTCAAACCTGCTAAAGAAATTGACTCTACATTGTATAAGAACTTATTTGTG  
a N I F K N C L K E I D S T L Y K N L F V - 1860  
1861 GATAAGAATATGAAGTATATCCAAACAGAAGATGTTCAGGTCTGTCACTGGAAGAACAA  
a D K N M K Y I P T E D V S G L S L E E Q -  
1921 TTGAGGAGGTTGCAAGAACGAACTTGTAAAGTGTGTATGGACAAAGAAGTTCTGT  
a L R R L Q E E R T C K V C M D K E V S V - 1980  
1981 GTATTATTCCCTTGCGGTCACTGGTAGTATGCCAGGAATGTGCCCTTCTCTAAAGAAA  
a V F I P C G H L V V C Q E C A P S L R K - 2040  
2041 TGCCCTATTTGCAGGGTATAATCAAGGGTACTGTTCGTACATTCTCTTAAGAAA  
a C P I C R G I I K G T V R T F L S \* - 2100  
2101 ATAGTCTATTTAACCTGCATAAAAGGTCTTAAATATTGTGAACTGTGAAGCC  
a -

Fig. 3 (page 6 of 7)

## HUMAN hiap-2

ATCTAAAGTAAAAGGGAATTAGGTTTCAATTACATTCAATGTTCTAGCTGC 2220  
2161 - - - - + - - - - + - - - - + - - - - + - - - - + 2220

a

TTGGTACTAATACTTGTTCTGAAAAGATGGTATCATATTTAATCTGTGTT 2280  
2221 - - - - + - - - - + - - - - + - - - - + - - - - + 2280

a

TATTTACAAGGGAAAGATTATGTTTGTTGAACCTATATTAGTATGTGTACCTAAGGG 2340  
2281 - - - - + - - - - + - - - - + - - - - + - - - - + 2340

a

AGTAGCGCTCXCTGCTTGTTATGCATCATTCAAGGAGTTACTGGATTGTGTCTTCAG 2400  
2341 - - - - + - - - - + - - - - + - - - - + - - - - + 2400

a

AAAGCTTTGAAAXACTAAATTATAGTGTAGAAAGAACTGGAAACCGGAACCTCTGGAGTT 2460  
2401 - - - - + - - - - + - - - - + - - - - + - - - - + 2460

a

CATCAGAGTTATGGTGCCGAATTGTCTTGTTGCTTCACTTGTGTAAATAAGGA 2520  
2461 - - - - + - - - - + - - - - + - - - - + - - - - + 2520

a

TTTTCTCTTATTCTACCCCTAGTTGTGAGAACATCTCAATAAGTGCTTTAAAG 2580  
2521 - - - - + - - - - + - - - - + - - - - + - - - - + 2580

a

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# MOUSE xiap

SEQ ID NO:9

1 GACACTCTGGGGGGGGCCCTCCCTGGAACCTCCCTCGGAACCGTCGCC 60

a

61 Gggggcctttagttaggactggactggcttggggaaaacgtggacaagtccatttcca 120

a

121 GAGAAGATGACTTTAACAGTTGAAGGAACTAGAACTTTGTACTTGCAGACCAA 180

SEQ ID NO:10 a

181 AACGATGAAAGAATTGTAGAAGAGTTAATAGATTAACATTTGCTTAACTTCCCAAGT 240

a

K D E E F V E E F N R L K T F A N F P S -

241 AGTAGTCCTGTTCAGCATCAACATGGCGGAGCTGGTTCTTATACCGGTGAAGGA 300

a

S S P V S A S T L A R A G F L Y T G E G -

301 GACACCGTTGCAATGTTCACTGTCATGGCGCAATAGATAGATGGCAGTATGGAGACTCA 360

a

D T V Q C F S C H A A I D R W Q Y G D S -

Fig. 4 (page 1 of 6)

## MOUSE xiap

361 GCTGTTGGAAGACACAGGAGAATATCCCCAAATGCGATTATCAATGGTTTATT 420  
- - - - + - - - + - - - + - - - + - - - + - - - + -  
a A V G R H R R I S P N C R F I N G F Y F -  
421 GAAAATGGTGCTGCACAGGTCTACAATCCTGGTATCCAAATGCCAGTACAATCTGAA 480  
- - - - + - - - + - - - + - - - + - - - + - - - + -  
a E N G A A Q S T N P G I Q N G Q Y K S E -  
481 AACTGTGTGGAAATAGAAATCCTTTGCCCTGACAGGCCACCTGAGACTCATGCTGAT 540  
- - - - + - - - + - - - + - - - + - - - + - - - + -  
a N C V G N R N P F A P D R P P E T H A D -  
541 TATCTCTTGAGAACTGGACAGGTTGAGATATTAGACACCCATACCCGAGGAACCT 600  
- - - - + - - - + - - - + - - - + - - - + - - - + -  
a Y L L R T G Q V V D I S D T I Y P R N P -  
601 GCCATGTGTAGTGAAGAACCCAGATGAACTTCAGAACTGGCCGGACTATGCTCAT 660  
- - - - + - - - + - - - + - - - + - - - + - - - + -  
a A M C S E E A R L K S F Q N W P D Y A H -  
661 TTAACCCCCAGAGAGTTAGCTAGTGTGGCCTACTACACAGGGCTGTGATCAACTG 720  
- - - - + - - - + - - - + - - - + - - - + - - - + -  
a L T P R E L A S A G L Y Y T G A D D Q V -

Fig. 4 (page 2 of 6)

## MOUSE xiap

721 CAATGCTTGTGTTGGGGAAACTGAAAATTGGGAACTCGCTGATCGTGCCGGTCA  
a Q C F C C G G K L K N W E P C D R A W S - 780  
GAACACAGGAGACACTTCCCAATTGCTTGTGGGGGGAACTTAATGTTCGA  
781  
a E H R R H F P N C F F V L G R N V N V R - 840  
AGTGAATCTGGTGTGAGTTCTGATAGGAATTCCCAATTCAACAACTCTCCAAGAAAT  
841  
a S E S G V S S D R N F P N S T N S P R N - 900  
CCAGCCATGGCAGAATATGAAAGCACGGATCGTTACTTTGGAACATGGATATACTCAGTT  
901  
a P A M A E Y E A R I V T F G T W I Y S V - 960  
AACCAAGGAGCAGCTTGCAAGAGCTGGATTATGCTTAGGTGAAGGGATAAGTGAAG  
961  
a N K E Q L A R A G F Y A L G E G D K V K - 1020  
TGCTTCCACTGTGGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAAG  
1021  
a C F H C G G G L T D W K P S E D P W D Q - 1080

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## MOUSE xiap

CATGCTAAGTGCTACCCAGGGTGCAAATACCTATTGGATGAGAAGGGCAAGAATATA  
1081 - - - + - - - + - - - + - - - + - - - + - - - + - - - + 1140

a H A K C Y P G C K Y L L D E K G Q E Y I -

AATAATATTCACTTAACTTACCCATCCACTTGAGGAATCTTGGAAGAACTGCTGAAACAA  
1141 - - - + - - - + - - - + - - - + - - - + - - - + - - - + 1200

a N N I H L T H P L E E S L G R T A E K T -

CCACCGCTAACTAAAAATCGATGATACCATCTCCAGAATCCTATGGTGCAAGAAGCT  
1201 - - - + - - - + - - - + - - - + - - - + - - - + - - - + 1260

a P P L T K K I D D T I F Q N P M V Q E A -

ATACGAATGGGATTAGCTTCAGGACCTTAAGAAAACAAATGGAAGAAAAATCCAAACA  
1261 - - - + - - - + - - - + - - - + - - - + - - - + - - - + 1320

a I R M G F S F K D L K K T M E E K I Q T -

TCCGGGAGCAGCTATCACTTGAGGTCTGATGAGATCTGTGAGTGCTCAGAAA  
1321 - - - + - - - + - - - + - - - + - - - + - - - + - - - + 1380

a S G S S Y L S L E V L I A D L V S A Q K -

GATAATAACGGAGGATGAGTCAGTCAGTCAGAAAGACATAGTACTGAGAG  
1381 - - - + - - - + - - - + - - - + - - - + - - - + 1440

a D N T E D E S S Q T S L Q K D I S T E E -

Fig. 4 (page 4 of 6)

## MOUSE xiap

1441 CAGCTAAGGGCCTACAGAGGAGAAGCTTCCAAATCTGTATGGATAGAAATATGCT 1500  
a Q L R R L Q E E K L S K I C M D R N I A -  
1501 ATCGTTTTCTCCTTGACATCTGGCACTTGTAACAGTGTGAGAAGCAGTGAC 1560  
a I V F F P C G H L A T C K Q C A E A V D -  
1561 AAATGTCATGTCCTACACCGTCATTACGTTCAACCAAAATTATGCTTAGTGG 1620  
a K C P M C Y T V I T F N Q K I F M S \* -  
1621 GGCACCCACATGTTATGTTCTTGCTCTAATTGAATGGATGTGTAATGGAGCGAACTTAAG 1680  
a -  
1681 TAATCCTGCATTTGCATTCCTAGCATCCTGCTGTTCCAAATGGAGACCAATGCTAAC 1740  
a -  
1741 AGCACTGTTCCGTCTAACATTCAATTCTGGATCTTCGAGTTATCAGCTGTATCATT 1800  
a -

Fig. 4 (page 5 of 6)

MOUSE xiap

Fig. 4 (page 6 of 6)

# M-hiap-1

SEQ ID NO:39

1 GAATTCCGGAGACCTACCCCCGGAGATCAGAGGTCA TGCTGGCTTCAGAGCCTAG 60  
61 GAACTGGGCTGCGGTATCAGCCTAGCAGTAAACCGACCAGAACCCATGCACAAACTAC 120  
121 ATCCCCAGAGAAAGACTTGTCCCTTCCCTGTCACTCACCATGAACATGGTTCAA 180

SEQ ID NO:40

M N M V Q -

181 GACAGCGCCTTCTAGCCAAGCTGATGAAGAGTGCTGACACCTTGACTGAAGTATGAC 240  
D S A F L A K L M K S A D T F E L K Y D -

241 TTTCCCTGTGAGCTGTACCGATTGTCACCGTATTCA GCTTTCCCAGGGAGTTCCTGTG 300  
F S C E L Y R L S T Y S A F D R G V P V -

301 TCAGAAAGGAGTCTGGCTCGTGGCTTTACTACACTGGTGCCAATGACAAGGTCAA 360  
S E R S I A R A G F Y Y T G A N D K V K -

361 TGCTTCTGTGCGCTGATGCTAGACAACCTGGAAACAAGGGACAGTCCCATGGAGAAG 420  
C F C C G L M I D N W K Q G D S P M E K -

Fig. 5 (page 1 of 6)

### M-hiap-1

421 CACAGAAAGTGTACCCCAGCTGCAACTTGTACAGACTTGAAATCCAGCCAACAGTCTG 480  
H R K L Y P S C N F V Q T L N P A N S L -  
GAAGCTAGTCTCGGCCTCTCTTCCACGGCGATGAGCACCATGCCCTTGAGCTT  
481 E A S P R P S L P S T A M S T M P L S F - 540  
GCAAGTTCTGAGAATACTGGCTATTCACTGGCTTACTCGAGCTTCCCTCAGACCT  
541 A S S E N T G Y F S G S Y S S F P S D P - 600  
GTGAACTTCCGAGCAAATCAAGATTGTCTGCTTGTGAGCACAAAGTCCCTACCACTTGCA  
601 V N F R A N Q D C P A L S T S P Y H F A - 660  
ATGAAACACAGAGAAGGCCAGATTACTCACCTATGAAACATGGCCATTGTCTTCTGTCA  
661 M N T E K A R L L T Y E T W P L S F L S - 720  
CCAGCAAAGCTGGCCAAAGCAGGCTTACTACATAGGACCTGGAGATAAGAGTGGCCTGC  
721 P A K L A K A G F Y Y I G P G D R V A C - 780

Fig. 5 (page 2 of 6)

M-hiap-1

### M-hiap-1

TTATCTACGTCAGACTCCCCAGAAGATGAGAATGCAGACGCAGCAATCGTGCATTGGC  
1201 - +-----+-----+-----+-----+-----+-----+-----+-----+ 1260  
L S T S D S P E D E N A D A A I V H F G -

CCTGGAGAAAGTCCGAGATGTGCTCATGATGAGCACGCCCTGGTAAAGCACCCRTG  
1261 - +-----+-----+-----+-----+-----+-----+-----+-----+ 1260  
P G E S S E D V V M M S T P V V K A A L -

GAATGGGCTTCAGTAGGAGCCTGGTGGAGACAGACGGTTCAGTGGCAGATCCTGGCCACT  
1321 - +-----+-----+-----+-----+-----+-----+-----+-----+ 1320  
E M G E S R S L V R Q T V Q W Q I L A T -

GGTGAGAACTACAGGACCGTCACTGACCTCGTTAGGCTACTCGATGAGAACGGAG  
1381 - +-----+-----+-----+-----+-----+-----+-----+-----+ 1380  
G E N Y R T V S D L V I G L L D A E D E -

ATGAGAGAGGAGCAGATGGAGCAGGGCCGAGGAGGAGTCAGATGATCTAGCACTA  
1441 - +-----+-----+-----+-----+-----+-----+-----+-----+ 1500  
M R E E Q M E Q A A E E E S D D L A L -

ATCCGGAAAGAACAAATGGTCTTCCAACATTGACGTGTGACACCCAATGCTGTAT  
1501 - +-----+-----+-----+-----+-----+-----+-----+-----+ 1560  
I R K N K M V L F Q H L T C V T P M L Y -

Fig. 5 (page 4 of 6)

## M-hiap-1

TCCTCCTAAGTGCAAGGCCATCACTGAAACAGGAGTGCAATGCTGTGAAACAGAACCA  
1561 ---+---+---+---+---+---+---+---+---+---+---+---+---+ 1620  
C L L S A R A I T E Q E C N A V K Q K P -  
  
CACACCTTACAAGCAAGCACACTGATTACTGTGTAGCAAAAGAACACTGCAGCA  
1621 ---+---+---+---+---+---+---+---+---+---+---+---+ 1680  
H T L Q A S T L I D T V L A K G N T A A -  
  
ACCTCATTCAGAAACTCCCTCGGAAATTGACCTGCGTTATACAGAGATATTTGTG  
1681 ---+---+---+---+---+---+---+---+---+---+---+ 1740  
T S F R N S L R E I D P A L Y R D I F V -  
  
CAACAGGACATTAGGAGTCTTCCCCACAGATGACATTGCAGCTCTACCAATGGAAGAACAG  
1741 ---+---+---+---+---+---+---+---+---+---+---+ 1800  
Q Q D I R S L P T D D I A A L P M E E Q -  
  
TTGGGGCCCTCCCGAGGACAGAATGTGTAAAGTGTGTATGGACCGAGAGGTATCCATC  
1801 ---+---+---+---+---+---+---+---+---+---+---+ 1860  
L R P L P E D R M C K V C M D R E V S I -  
  
GTGTTCATTCCTGTGGCCATCTGGTCGTGTGCAAAGACTGCCCTCTGAGGAAG  
1861 ---+---+---+---+---+---+---+---+---+---+---+ 1920  
V F I P C G H L V V C K D C A P S L R K -

Fig. 5 (page 5 of 6)

M-hiap-1

Fig. 5 (page 6 of 6)

M-hiap-2

SEQ ID NO:41

1 CTGTGGAGATCTATGTCCTAAGGGAGAACTCCATCTGGAGTTAAGGGTCA 60  
GAAATACTTAACTACTCATGGACAKRACGTCTCCAGAGACTCGCCAAAGGTACCTTA  
61 CACCCRAAACTTAAACGTATAATGGAGAAGAGCACAATCTGTCAATTGGACAAAGGA 120

SEQ ID NO:42

121 M E K S T I L S N W T K E - 180

181 GAGCCGAAGAAAAATGAAGTTGACTTTCTGTGTGAACTCTACCGAATGTCTACATATTC  
S E E K M K F D F S C E L Y R M S T Y S - 240

241 AGCTTTCCAGGGAGTCTCTGTCTCAGAGAGGACTCTGGCTCGTGCTGGCTTTATA  
A F P R G V P V S E R S L A R A G F Y Y - 300

301 TACAGGTGTGAATGACAAGTCAAGTCTCTGCTGTGGCCTGATGTGGATAACTGGAA 360  
T G V N D K V K C F C C G L M L D N W K -

361 ACAAGGGACAGTCCTGTGAAAGCACAGACAGTTCTATCCAGCTGCAGCTTGTACA  
Q G D S P V E K H R Q F Y P S C S F V Q - 420

## M-hiap-2

421 GACTCTGCTTCAGCCAGTCAGTCCTCCATCTAAGAATATGTCCTCTGTGAAAGTAG  
T L L S A S I Q S P S K N M S P V K S R - 480

481 ATTTGCACATTCGTCACCTCTGAAACGAGGTGGCATTCACTCCAACCTGTGCTCTAGCCC  
F A H S S P L E R G G I H S N L C S S P - 540

541 TCTTAATTCTAGAGCAGTGGAAAGACTTCTCATCAAGGATGGATCCCCTGCAGCTATGCCAT  
L N S R A V E D F S S R M D P C S Y A M - 600

601 GAGTACAGAAGAGGCCAGATTCTTACTTACAGTATGTGGCCTTAAAGTTCTGTCAACC  
S T E E A R F L T Y S M W P L S F L S P - 660

661 AGCAGAGCTGGCCAGAGCTGGCTTCTATTACATAGGGCCTGGAGACAGGGTGGCCTGTT  
A E L A R A G F Y Y I G P G D R V A C F - 720

721 TGCCTGTGGTGGAAACTGACCAACTGGGAACCAAAGGATTATGCTATGTCAAGACCCG  
A C G G K L S N W E P K D Y A M S E H R - 780

Fig. 6 (page 2 of 6)

## M-hiap-2

CAGACATTTCCCCACTGTCCTTCTGGAAATACTTCAGAACACAGAGGTTAGTAT  
781 - - - - + - - - + - - - + - - - + - - - + - - - + - - - + 840  
R H F P H C P F L E N T S E T Q R F S I -

ATCAAATCTAAGTATGCAGACACACTCTGCTCGATTGAGGACATTCTGTACTGGCCACC  
841 - - - - + - - - + - - - + - - - + - - - + - - - + - - - + 900  
S N L S M Q T H S A R L R T F L Y W P P -

TAGTGTTCCTGTCAGCCGAGCAGCTGCAAGTGTGATTCTATTACGGATCGCRA  
901 - - - - + - - - + - - - + - - - + - - - + - - - + - - - + 960  
S V P V Q P E Q L A S A G F Y Y V D R N -

TGATGATGTCAGTGCCTTGTGATGGCTTGAGATGTTGGAACCTGGAGATGA  
961 - - - - + - - - + - - - + - - - + - - - + - - - + - - - + 1020  
D D V K C L C C D G G L R C W E P G D D -

CCCCCTGGATAGAACACGCCAATGGTTCCAAGGTGTGAGTTCTGATAACGGATGAAGGG  
1021 - - - - + - - - + - - - + - - - + - - - + - - - + - - - + 1080  
P W I E H A K W F P R C E F L I R M K G -

TCAGGAGTTGTGATGAGATCAAGCTAGATATCCTCATCTTCTTGAGCCAGCTGTTGTC  
1081 - - - - + - - - + - - - + - - - + - - - + - - - + - - - + 1140  
Q E F V D E I Q A R Y P H L L E Q L L S -

Fig. 6 (page 3 of 6)

M-hiap-2

CACTTCAGACACCCAGGAGAAGAAATGCTGACCCCTACAGAGACAGTGGTGCATTTGG  
1141 - +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1200  
T S D T P G E E N A D P T E T V V H F G -

CCCTGGAGAAAGTTCGAAAGATGTCGTCATGATGAGCAGCAGCCTGGTTAACGAGCTT  
1201 - +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1260  
P G E S S K D V V M M S T P V V K A A L -

CGAAATGGGCTTCAGTAGGAGCCTGGTGAGACAGACGGTTCAAGCCAGATCCTGGCAC  
1261 - +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1320  
E M G F S R S L V R Q T V Q R Q I L A T -

TGGTGAGAACTACAGGACCGTCAATGATATTGTC'CACTACTTGAATGCTGAAGATGA  
1321 - +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1380  
G E N Y R T V N D I V S V L L N A E D E -

GAGAAGAGAAGAGGAGAAGGAAGACAGACTGAAGAGATGGCATCAGGTGACTTCACT  
1381 - +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1440  
R R E E K E R Q T E E M A S G D L S L -

GATTCGGAAGAATAGAATGGCCCTCTTCAACAGTGTGACACATGTCCTTCTATCCTGGA  
1441 - +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1500  
I R K N R M A L E Q Q L T H V L P I L D -

Fig. 6 (page 4 of 6)

## M-hiap-2

TAATCTTCTGAGGCCAGTGTAAACAAACAGGACATGATATTAGACAGAAC  
1501 - - - - + - - - + - - - + - - - + - - - + - - - + 1560  
N L L E A S V I T K Q E H D I I R Q K T -  
ACAGATAACCCTTACAAGCAAGAGACTTATTGACACCGTTAGTCAGGAATGCTGC  
1561 - - - + - + - + - + - + - + - + - + - + - + 1620  
Q I P L Q A R E L I D T V L V K G N A A -  
AGCCAACATCTCAAAACTCTCTGAAGGGATTGACTCCACGGTATATGAAACTTATT  
1621 - - - + - + - + - + - + - + - + - + - + - + 1680  
A N I F K N S L K G I D S T L Y E N L F -  
TGTGGAAAGAATAATGAAGTATTCACAGAACAGACGGTTCAAGGCTTGTCAATTGGAAGA  
1681 - - - + - + - + - + - + - + - + - + - + - + 1740  
V E K N M K Y I P T E D V S G L S L E E -  
GCAGTTGGGAGATTACAAAGAACGAACTTGCAAGTGTGTATGGACAGAGGGTTTC  
1741 - - - + - + - + - + - + - + - + - + - + - + 1800  
Q L R R L Q E E R T C K V C M D R E V S -  
TATTGTGTTCAATTCCGTGGTCATCTAGTAGTGTCTGCCAGGAATGTGCCCTTCTCTAAG  
1801 - - - + - + - + - + - + - + - + - + - + - + 1860  
I V F I P C G H L V V C Q E C A P S L R -

Fig. 6 (page 5 of 6)

M-hiap-2

Fig. 6 (page 6 of 6)

## Alignment of BIR (Baculoviral IAP Repeats) Domains

Fig. 7

|                    | Baculovirus  | Cydia pomonella  |
|--------------------|--|--|
|                    | Cp_iap   | Orgyia pseudotsugata                                   |
|                    | Op_iap   |  |
| Human              |  |  |
| xiap               | IAP on X chromosome  |  |
| hiap1, hiap2       | two different human IAP genes  |  |
| Mouse              |  |  |
| m-xiap             | mouse homologue of human xiap gene   |  |
| Insect             |  |  |
| diap               | Drosophila IAP gene, not clearly a homologue of xiap or hiap   |  |
| note on consensus: | The consensus line represents amino acids or very similar amino acids which are present in 14 of the 19 BIR sequences at each position. Capitalized residues are those that are in the consensus sequence. |  |
|                    | 1  | 68   |
| SEQ ID NO:11       | Op_iap-1   | kaaRlgTytn WPvqf.leps rMaasGFYyl GrgDevrCaf Ckveitnwrv |
| SEQ ID NO:14       | Cp_iap-1   | eevRlnTFek WPvsf.lspe tMAknGFYyl GrsDevrCaf CkveimrWke |
| SEQ ID NO:15       | diap-2   | gEdpaadHkk waPqCpFV                                    |
| SEQ ID NO:16       | m-xiap-1   | eanRLvTFkd WPnpn.ilpq aLAkAGFYYl nrlDhvKcvw CngviakWeK |
| SEQ ID NO:17       | xiap-1   | ndnafeeHkr ffpqCpFV                                    |
| SEQ ID NO:18       | hiap1-1  | efnRLkTFan Fpssspvss tlArAGFLyt GegDtVqCfs             |
| SEQ ID NO:19       | hiap2-1  | chaaidrWQy gdsavgrHrr isPnCrFI                         |
| SEQ ID NO:20       | m-xiap-2   | efnRLkTFan Fpssspvss tlArAGFLyt GegDtVqCfs             |
| SEQ ID NO:21       | xiap-2   | chaavdrWQy gdsavgrHrr vsPnCrFI                         |
| SEQ ID NO:22       | hiap1-2  | elyRMstYst Fpaggpvsas tlArAGFLyt GegDtVqCfs            |
| SEQ ID NO:23       | hiap2-2  | elaSAGLYyt GddQvqCfc                                   |
| SEQ ID NO:24       | m-xiap-3   | earRLksFqn Wpdyahlptr elASAGLYyt GddQvqCfc             |
| SEQ ID NO:25       | xiap-3   | eeARLkFqn WPdyahlptr elASAGLYyt GddQvqCfc              |
| SEQ ID NO:26       | hiap1-3  | enARLlTFqt WP.llflspt dLArAGFYYi GpgDrvAcFa            |
| SEQ ID NO:27       | hiap2-3  | CGgk1snWep kDnamseHlr                                  |
| SEQ ID NO:28       | Op_iap-2   | earRLlTFhm WP.llflsps elArAGFYYi GpgDrvAcFa            |
| SEQ ID NO:29       | Cp_iap-2   | CGgk1snWep kDdamseHrr hfpnCpFI                         |
| SEQ ID NO:30       | diap-3   | yearIvTFgt Wiysv..nke qLArAGFyAl GegDkVkCfH            |
| SEQ ID NO:31       | diap-1   | Cgg1tdwkp sEdpwdqHak cyPgCkYl                          |
| Consensus          |  |  |
|                    | --RL-TF--  | waPqCpFV   |
|                    | WP-----  |  |
|                    | -LA-AGFYV-   |  |
|                    | G--D-V-CF-   |  |
|                    | C-----W--  |  |
|                    | -D-----H--   |  |
|                    | --P-C-FV   |  |

Fig. 8 (page 1 of 5)

Fig. 8 (page 2 of 5)

| BIR 3 |             |
|-------|-------------|
| 301   | cp-iap      |
|       | qrPEQOMADAG |
|       | FFYtGyGDnt  |
|       | KCFyCdgGLk  |
|       | dWepeDvPWe  |
|       | QHvrWFdrCa  |
|       | diap        |
|       | qpasalaQAG  |
|       | LYYqk1Gdqv  |
|       | rCFhCniGLr  |
|       | sWqkeDEPwf  |
|       | eHAKWSPkCq  |
|       | m-xiap      |
|       | VnKEQlARAG  |
|       | FyalGeGDKV  |
|       | KCFhCggGLt  |
|       | dwkpsEDPwD  |
|       | QHAKWYpgCk  |
|       | xiap        |
|       | VnPEQLASAG  |
|       | FYYvGnsDdv  |
|       | KCFCCdGGLr  |
|       | cWesgDDPwv  |
|       | QHAKWFPrCe  |
|       | hiap1       |
|       | VqPEQLASAG  |
|       | FYYvGRsDdv  |
|       | KCFgCdgGLr  |
|       | cWesgDDPwv  |
|       | eHAKWFPrCe  |
|       | hiap2       |
|       | V--EQLA-AG  |
|       | FYY-G-GD-V  |
|       | KCF-C-GGL-  |
|       | -W--DDPW-   |
|       | QHAKWFPrCe  |
|       | consensus   |
| 350   |             |
| 351   |             |
|       | cp-iap      |
|       | yvqlvKGrdY  |
|       | VgkVit...   |
|       | diap        |
|       | FullakGpay  |
|       | VsevLattaa  |
|       | nassqpaTap  |
|       | aptlq...    |
|       | m-xiap      |
|       | yIldeKGQEy  |
|       | Innlhlthp.  |
|       | LeEslgrTae  |
|       | kt...       |
|       | xiap        |
|       | yLlegKGQEy  |
|       | Innlhlths.  |
|       | LeEclvrTte  |
|       | kt...       |
|       | hiap1       |
|       | yLirkKGQEy  |
|       | IrqVqgasypH |
|       | LLEGqlLsTsD |
|       | spgdenaess  |
|       | ihlePgedh   |
|       | hiap2       |
|       | FlirmKGQEF  |
|       | VdeIqgryph  |
|       | LLEGqlLsTsD |
|       | ttgeeenadpp |
|       | ihfgPgess   |
|       | consensus   |
|       | YL---KGQEy  |
| 400   |             |
| 401   |             |
|       | cp-iap      |
|       | ..acVlpgE   |
|       | diap        |
|       | ..adVlmdEA  |
|       | pakeAltLgi  |
|       | dggyVrnaiq  |
|       | rKlissGcaf  |
|       | stldeLLhDi  |
|       | m-xiap      |
|       | kiddtifqnp  |
|       | mvqeAirMgf  |
|       | sfkdlkktme  |
|       | ekiIqtsGssy |
|       | lslevlLiadL |
|       | xiap        |
|       | riDdtifqnp  |
|       | mVqeAirMgf  |
|       | sfkdkikkime |
|       | ekiIqisGsnY |
|       | kslevlVadL  |
|       | hiap1       |
|       | seDaIMmntP  |
|       | vInaAvemGf  |
|       | srsIVkgtvG  |
|       | rKlalatGeny |
|       | rlvndlV1DL  |
|       | hiap2       |
|       | seDaVMmntP  |
|       | vVksAlleMgf |
|       | nrdlvKqtvI  |
|       | skIlttGeny  |
|       | ktvndivsA   |
|       | consensus   |
|       | --D-V---P   |
|       | -V--A--MGF  |
|       | -----VK---  |
|       | -KI---G--Y  |
|       | -----LV-DL  |
| 450   |             |

Fig. 8 (page 3 of 5)

Fig. 8 (sheet 4 of 5)

### Ring Zinc Finger

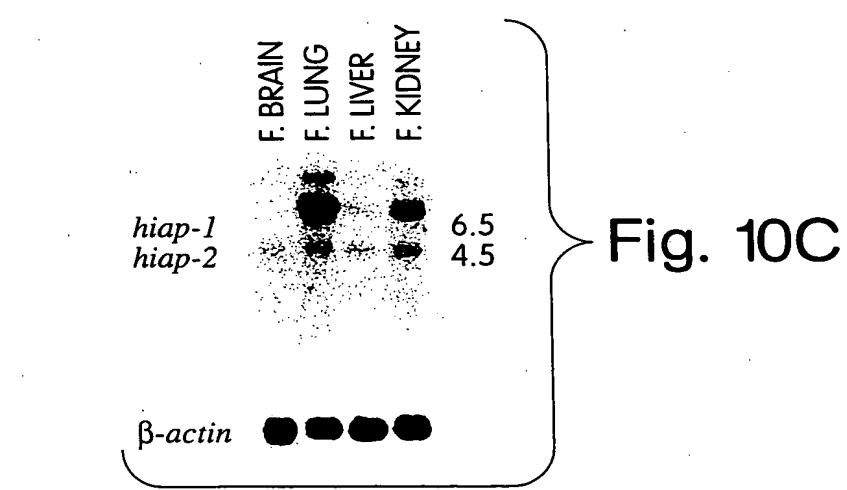
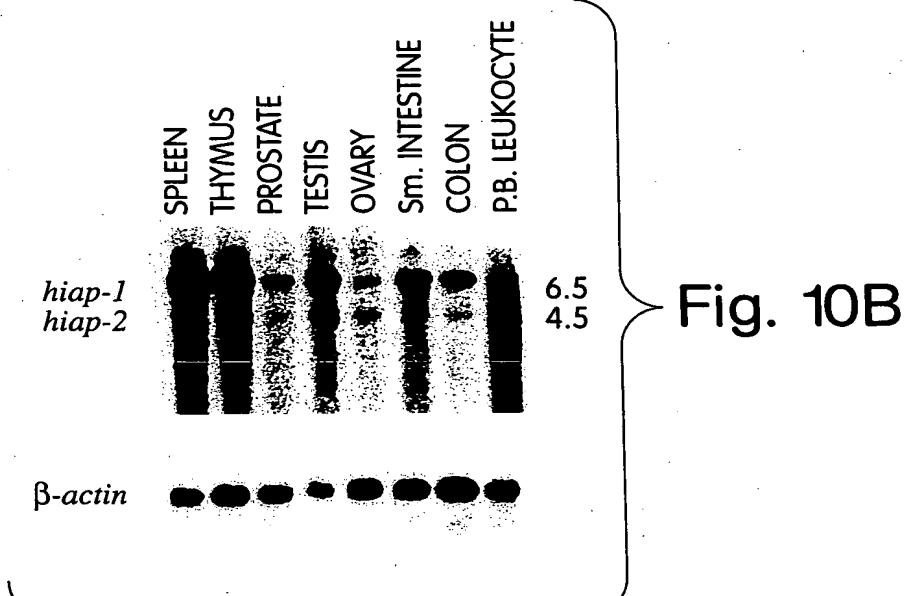
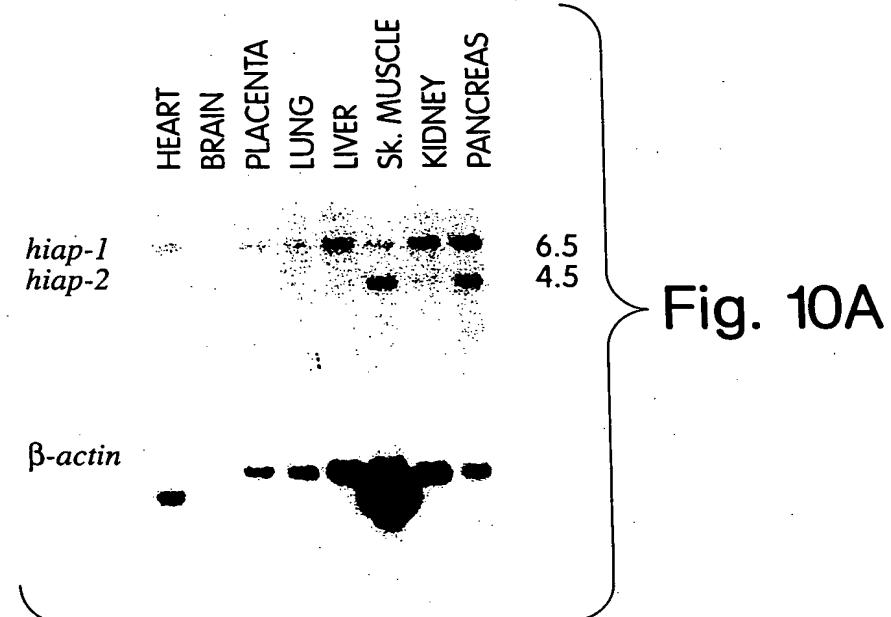
|           |              | 551         | 600         |
|-----------|--------------|-------------|-------------|
| cp-iap    | ...tki:... . | Ekepq       | veDskLICKIC |
| diap      | sniskitdei   | qkmsvstpng  | yveEcivcFV  |
| m-xiap    | .....        | .....k      | lkDarLICKVC |
| xiap      | .....        | .....k      | iDeEvgvvfl  |
| hiapl     | lyehlfvqgd   | ikyiptedvs  | disTEQlRR   |
| hiap2     | lyknlfvdkn   | mkyiptedvs  | LQEEKLskIC  |
| consensus |              |             | MDrnIaIVFf  |
|           |              |             | eISTEQlRR   |
|           |              |             | LQEEKLICKIC |
|           |              |             | MDrnIaIVFf  |
|           |              |             | lPEERTCKVC  |
|           |              |             | MDKEVsIVFI  |
|           |              |             | glsLEQlRR   |
|           |              |             | LQEERTCKVC  |
|           |              |             | MDKEVsIVFI  |
|           |              |             | L-EE-LCK-C  |
|           |              |             | MD-EV--VF-  |
|           |              | 601         | 635         |
| cp-iap    | PCGHvVaCak   | CAISVdkCPM  | DRKIVTsvlk  |
| diap      | PCGHlatCng   | CAPSvancPM  | vyFS.       |
| m-xiap    | PCGHlatCkq   | CAeavdkCPM  | DRadIkgfv   |
| xiap      | PCGHlvtCkg   | CytvITfngk  | tFLS*       |
| hiapl     | PCGHlVvCkd   | CAeavdkCPM  | iFMS*       |
| hiap2     | PCGHlVvCqe   | CAPS1rkCpi  | CytvITfkqk  |
| consensus | PCGHlVvCqe   | CAPIslrkCpi | ifMS*       |
|           | PCGHlV-C--   | CR-SV-KCPM  | CRstIkgtvr  |
|           |              | CR-I-----   | tFLS*       |
|           |              | -FLS-       |             |

Fig. 8 (sheet 5 of 5)

## Alignment of RZF (Ring Zinc Finger) Domains

|   |  |
|---|--|
| <b>Baculovirus</b>  |  |
| Cp_iap  | Cydia pomonella  |
| Op_iap  | Orgyia pseudotsugata   |
| <b>Human</b>  |  |
| xiap  | IAP on X chromosome  |
| hiap1, hiap2  | two different human IAP genes                                |
| <b>Mouse</b>  |  |
| m-xiap  | mouse homologue of human xiap gene                           |
| <b>Insect</b>   |  |
| diap  | Drosophila IAP gene, not clearly a homologue of xiap or hiap |
| <b>note on consensus:</b>   |  |
| The consensus line represents amino acids or very similar amino acids which are present in 6 of the 7 RZF sequences at each position. |  |
| Capitalized residues are those that are in the consensus sequence.  |  |
|   | 1  |
| SEQ ID NO:32  | hiap2  |
| SEQ ID NO:33  | hiap1  |
| SEQ ID NO:34  | m-xiap   |
| SEQ ID NO:35  | xiap   |
| SEQ ID NO:36  | diap   |
| SEQ ID NO:37  | Cp_iap   |
| SEQ ID NO:38  | Op_iap   |
| SEQ ID NO:1   | consensus  |
|   | 46   |
| Eqrrrlqger  | tckVCMdkev   |
| EqrllrpEer  | sIVFIPCGHl   |
| EqrllrqEek  | w Ckdcapsl   |
| EqrllrqEek  | rkCPic   |
| EqrrrlqEek  | atCkqCAeav   |
| EqrrrlqEek  | dkCPmc   |
| EqrllrqEek  | lCKICMdnni   |
| EqrllrqEek  | aIVFvPCGHl   |
| EqrllrqEek  | vtCkqCAeav   |
| EqrllrqEek  | dkCPmc   |
| EenrqlkDar  | lCKVCLdeev   |
| EenrqlkDar  | gVvFLPCGHl   |
| EenrqlkDar  | atCnqCApev   |
| EenrqlkDar  | anCPmc   |
| EkepgvEdsk  | lCKICYveec   |
| EkepgvEdsk  | IVCFvPCGHv   |
| EkepgvEdsk  | vaCakCALsv   |
| EkepgvEdsk  | dkCPmc   |
| aveaevaDdr  | lCKIClqack   |
| aveaevaDdr  | tCvFvPCGHv   |
| aveaevaDdr  | vaCgkCAagv   |
| aveaevaDdr  | ttCPvC   |
| E-----E--   | -CKICM-----  |
| E-----E--   | -V-F-PCGH-----   |
| E-----E--   | --C--CA-----   |
| E-----E--   | --CP-C-----  |

Fig. 9



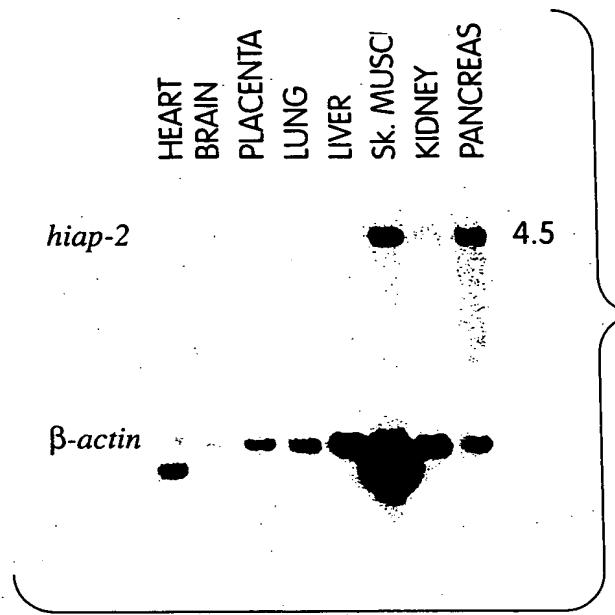


Fig. 11A

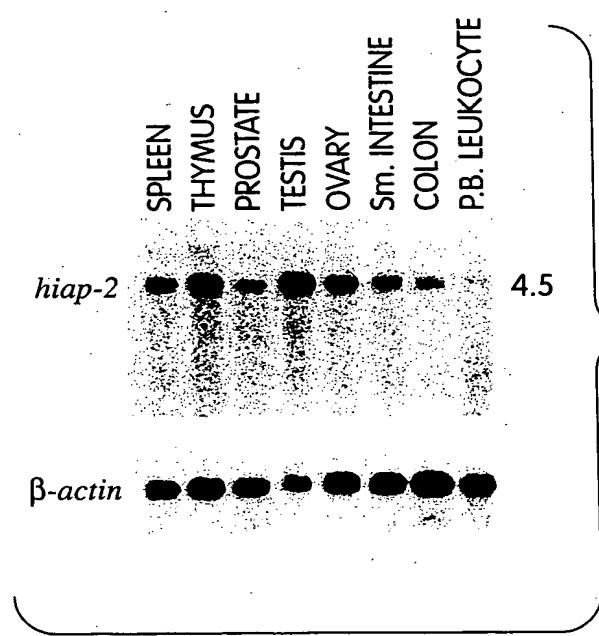


Fig. 11B

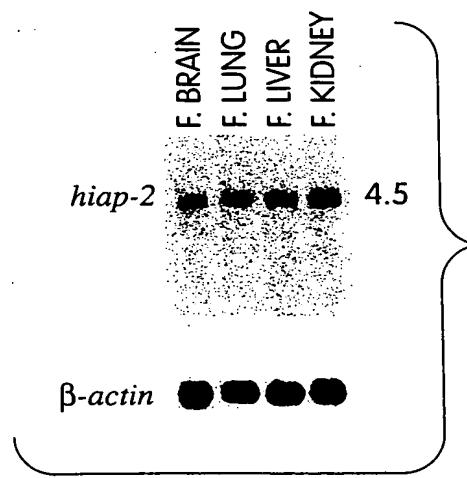
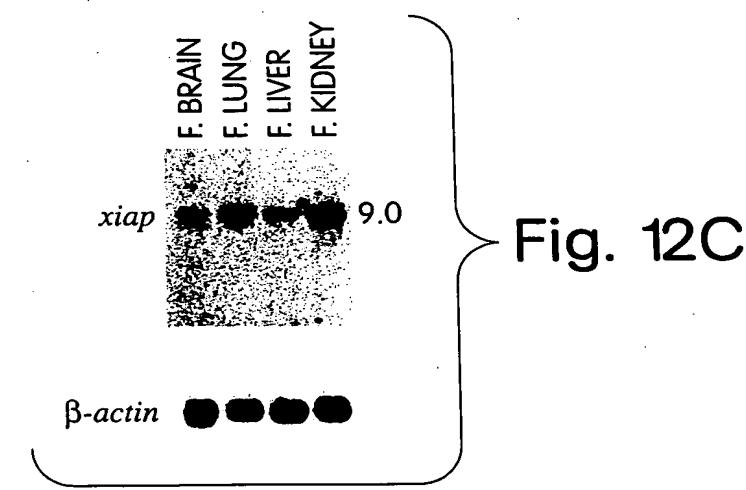
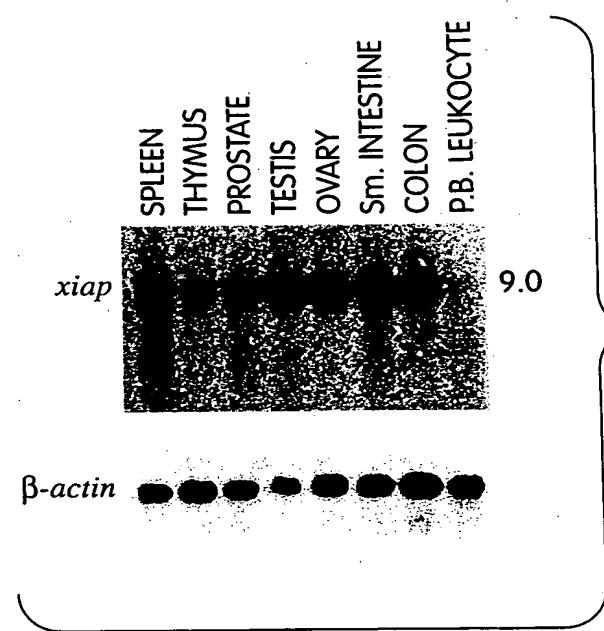
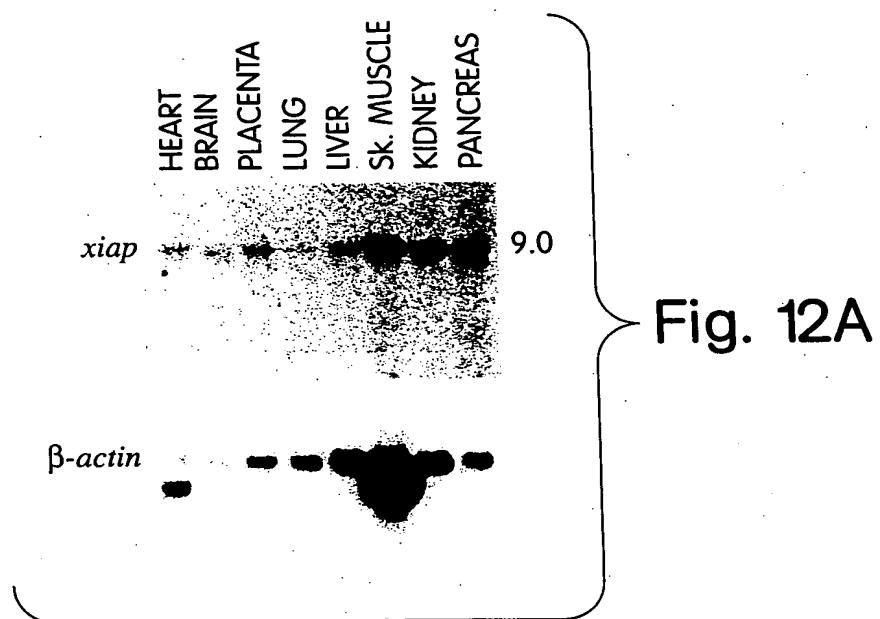


Fig. 11C



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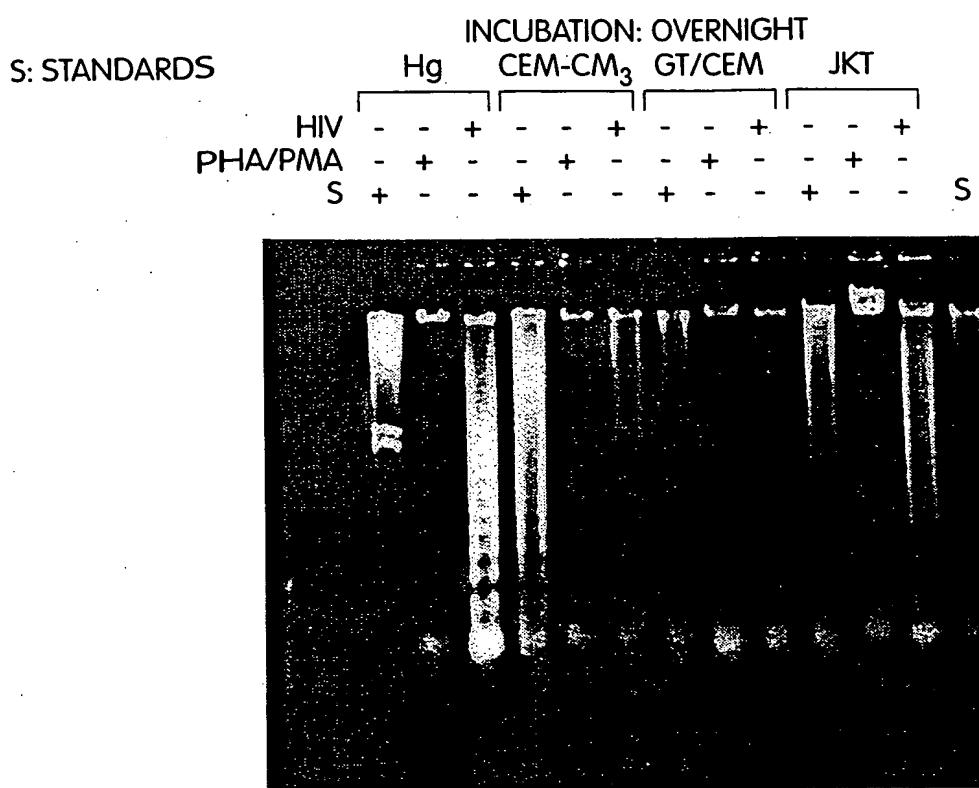


Fig. 13A

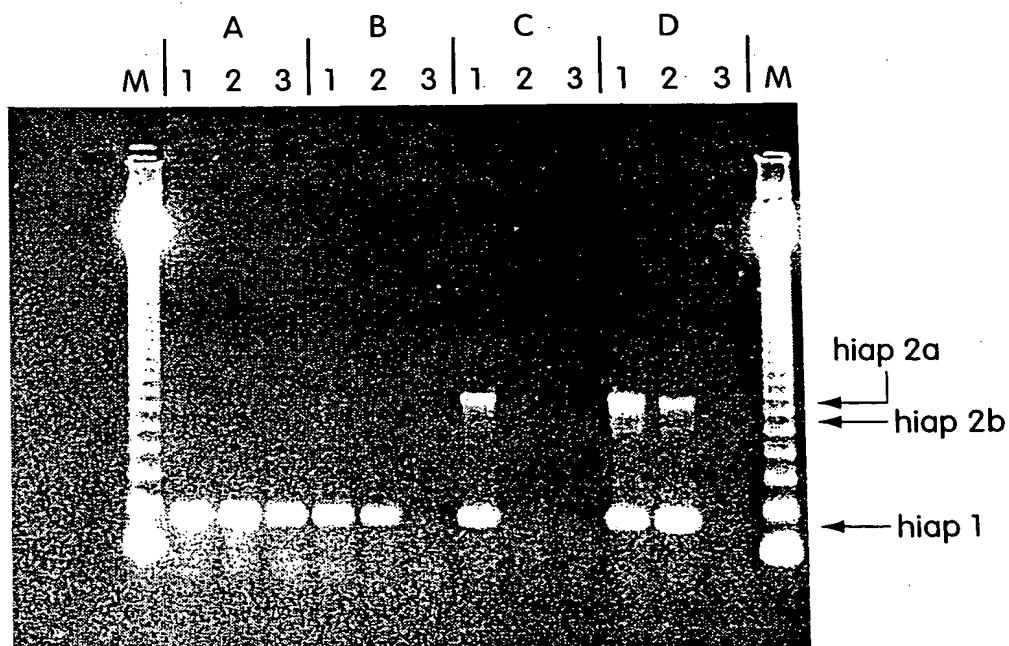


Fig. 13B

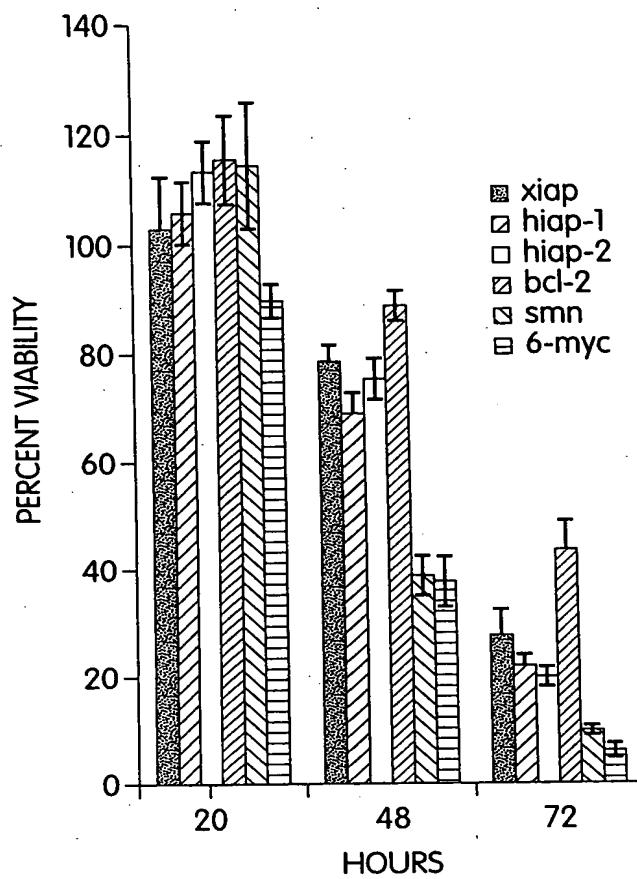


Fig. 14A

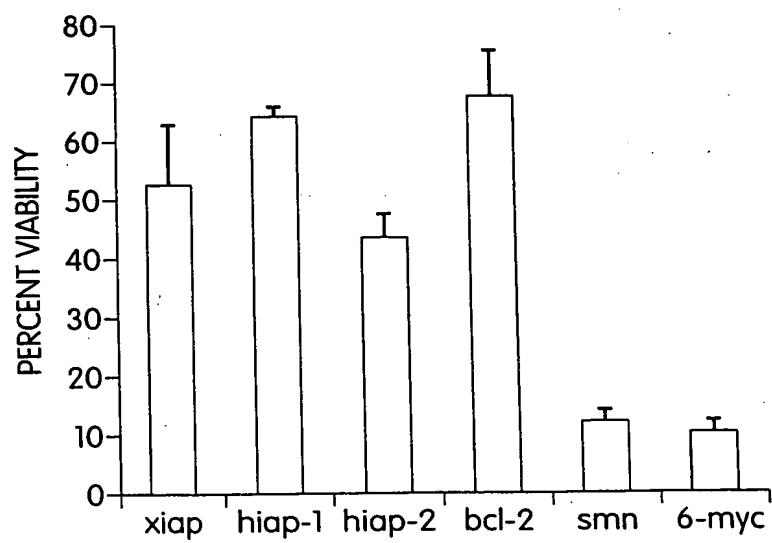


Fig. 14B

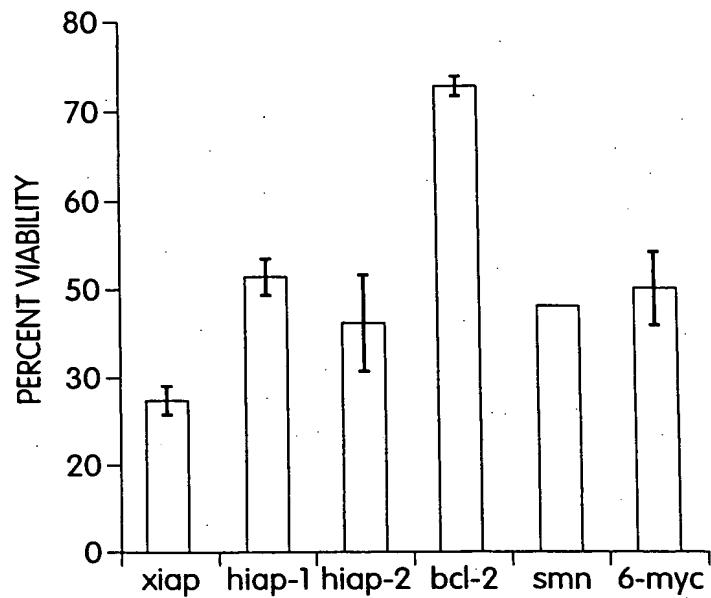


Fig. 14C

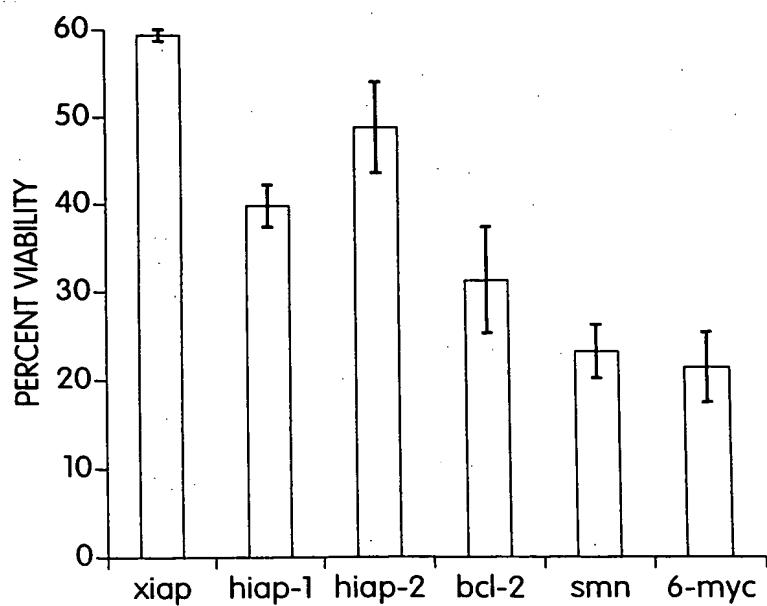


Fig. 14D